

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:57:52 ; Search time 31.07 seconds
(without alignments)
3253.332 Million cell updates/sec

Title: US-09-587-111-5
4004
Perfect score: 1 MTSPPSSPVFRLETLTGCGE.....EDEDGASEENVVPVQLQSN 764
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 133305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.unclassified:*
14: sp.vertebrate:*
15: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|--------------------|
| 1 | 4004 | 100.0 | 764 | 4 Q9Y5S1 | Q9Y5S1 homo sapien |
| 2 | 3945 | 98.5 | 764 | 4 Q9Y670 | Q9Y670 homo sapien |
| 3 | 3159 | 78.9 | 756 | 11 Q9WTR1 | Q9WTR1 mus musculu |
| 4 | 3051.5 | 76.2 | 761 | 11 Q9WUD2 | Q9WUD2 mus musculu |
| 5 | 3041.5 | 76.0 | 761 | 11 Q9QYH8 | Q9QYH8 rattus norv |
| 6 | 3028.5 | 75.6 | 762 | 11 Q9JMI8 | Q9JMI8 rattus norv |
| 7 | 1652 | 41.3 | 838 | 11 Q35433 | Q35433 rattus norv |
| 8 | 1652 | 41.3 | 838 | 11 Q9JMS7 | Q9JMS7 rattus norv |
| 9 | 1651.5 | 41.2 | 839 | 4 Q9H304 | Q9H304 homo sapien |
| 10 | 1648.5 | 41.2 | 839 | 4 Q9H0G9 | Q9H0G9 homo sapien |
| 11 | 1644.5 | 41.1 | 839 | 4 Q9H074 | Q9H074 homo sapien |
| 12 | 1636.5 | 40.9 | 839 | 4 Q9NY22 | Q9NY22 homo sapien |
| 13 | 1467 | 36.6 | 852 | 13 Q9DFS3 | Q9DFS3 gallus gall |
| 14 | 1467 | 36.6 | 871 | 4 Q9HBC0 | Q9HBC0 homo sapien |
| 15 | 1465.5 | 36.6 | 871 | 11 Q9ERZ8 | Q9ERZ8 rattus norv |
| 16 | 1464 | 36.6 | 871 | 4 Q9HBA0 | Q9HBA0 homo sapien |
| 17 | 1458.5 | 36.4 | 871 | 11 Q9ES76 | Q9ES76 mus musculu |
| 18 | 1457.5 | 36.4 | 871 | 11 Q9EPK8 | Q9EPK8 mus musculu |
| 19 | 1452.5 | 36.3 | 871 | 11 Q9EQZ4 | Q9EQZ4 mus musculu |

| | | | | | |
|-----|--------|------|------|-----------|--------------------|
| 20- | 1446.5 | 36.1 | 873 | 11 Q9ERZ7 | Q9ERZ7 mus musculu |
| 21 | 1442.5 | 36.0 | 778 | 11 Q9JMS6 | Q9JMS6 rattus norv |
| 22 | 1112.5 | 27.8 | 528 | 11 Q9Z182 | Q9Z182 rattus norv |
| 23 | 969 | 24.2 | 511 | 4 Q9H303 | Q9H303 homo sapien |
| 24 | 933 | 23.3 | 471 | 11 Q9JLMO | Q9JLMO rattus norv |
| 25 | 634 | 15.8 | 725 | 4 Q9H296 | Q9H296 homo sapien |
| 26 | 631 | 15.8 | 725 | 4 Q9H1D1 | Q9H1D1 homo sapien |
| 27 | 630 | 15.7 | 725 | 4 Q9H1D0 | Q9H1D0 homo sapien |
| 28 | 607.5 | 15.2 | 727 | 11 Q9R186 | Q9R186 rattus norv |
| 29 | 589 | 14.7 | 723 | 11 Q9J1P0 | Q9J1P0 rattus norv |
| 30 | 586 | 14.6 | 730 | 6 Q9XSM3 | Q9XSM3 oryctolagus |
| 31 | 584 | 14.6 | 723 | 11 Q9J1L2 | Q9J1L2 rattus norv |
| 32 | 579.5 | 14.5 | 729 | 4 Q9NOA5 | Q9NOA5 homo sapien |
| 33 | 469.5 | 11.7 | 769 | 5 Q9N3Y9 | Q9N3Y9 caenorhabd |
| 34 | 440.5 | 11.0 | 729 | 11 Q9J1J0 | Q9J1J0 mus musculu |
| 35 | 428.5 | 10.7 | 750 | 5 Q9VUD5 | Q9VUD5 drosophila |
| 36 | 414 | 10.3 | 900 | 5 Q61220 | Q61220 caenorhabd |
| 37 | 392.5 | 9.8 | 790 | 5 P90784 | P90784 caenorhabd |
| 38 | 364 | 9.1 | 937 | 5 Q17469 | Q17469 caenorhabd |
| 39 | 338 | 8.4 | 1123 | 5 Q9W3W0 | Q9W3W0 drosophila |
| 40 | 261 | 6.5 | 519 | 5 Q22374 | Q22374 caenorhabd |
| 41 | 255 | 6.4 | 1913 | 5 Q9GRV5 | Q9GRV5 caenorhabd |
| 42 | 233 | 5.8 | 904 | 5 Q9W0T5 | Q9W0T5 drosophila |
| 43 | 229 | 5.7 | 1453 | 5 Q9VMR4 | Q9VMR4 drosophila |
| 44 | 226.5 | 5.7 | 981 | 6 P79100 | P79100 bos taurus |
| 45 | 224.5 | 5.6 | 890 | 11 Q9QU09 | Q9QU09 mus musculu |

ALIGNMENTS

| RESULT | ID | PRELIMINARY: | PRT: | 764 AA. |
|-----------------------|---|---------------|-----------|-------------|
| Q9Y5S1 | Q9Y5S1 | | | |
| AC | Q9Y5S1 | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Created) | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Last sequence update) | | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | | | |
| DE | VANILLOID RECEPTOR-LIKE PROTEIN 1. | | | |
| GN | VRL-1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=9215558; PubMed=10201375; | | | |
| RA | Caterina M.J., Rosen T.A., Tomimaga M., Brake A.J., Julius D.; | | | |
| RT | "A capsaicin-receptor homologue with a high threshold for noxious heat."; | | | |
| RT | Nature. 398:436-441(1999). | | | |
| DR | EMBL: AF129112; AAD26363.1; -. | | | |
| DR | InterPro: IPR002110; -. | | | |
| DR | InterPro: IPR002111; -. | | | |
| DR | Pfam: PF00023; ank. 3. | | | |
| DR | PROSITE: PS50088; ANK_REPEAT. 1. | | | |
| DR | PROSITE: PS50297; ANK_REPEAT_REGION. 1. | | | |
| DR | SMART: SM00248; ANK. 1. | | | |
| DR | Receptor. | | | |
| SQ | SEQUENCE 764 AA: 85980 MW: A73E3696E70F91E9 CRC64: | | | |
| Query Match | 100.0%: | Score 4004: | DB 4: | Length 764: |
| Best Local Similarity | 100.0%: | Pred. No. 0: | | |
| Matches 764: | Conservative 0: | Mismatches 0: | Indels 0: | Gaps 0: |
| OY | 1 MTSPPSSPVFRLETLTGCGEADRGKIDFGSGLPNMFESQFQGEGRKFAPIRVNLNY 60 | | | |
| DB | 1 MTSPPSSPVFRLETLTGCGEADRGKIDFGSGLPNMFESQFQGEGRKFAPIRVNLNY 60 | | | |
| OY | 61 RKTGASQDPNFRDRLFNNAVSRGVPEDLAGLPYLSKTSKYLLTDSYETGSGTKTCL 120 | | | |
| DB | 61 RKTGASQDPNFRDRLFNNAVSRGVPEDLAGLPYLSKTSKYLLTDSYETGSGTKTCL 120 | | | |

| | | | |
|--------|--|---|------|
| QY | 121 | MKAVNLKEDGVNACILPLQLQIDRPSGNOPPLVNAQCTDDYRGSAHLIAIERKSLQCVK | 180 |
| QY | 121 | MKAVNLKEDGVNACILPLQLQIDRPSGNOPPLVNAQCTDDYRGSAHLIAIERKSLQCVK | 180 |
| Db | 121 | MKAVNLKEDGVNACILPLQLQIDRPSGNOPPLVNAQCTDDYRGSAHLIAIERKSLQCVK | 180 |
| QY | 181 | LLVENGANVHARACGRFFQKQSGTCFYFGLPLSLAACRQMDVSVYLENPHQPSLQA | 240 |
| Db | 181 | LLVENGANVHARACGRFFQKQSGTCFYFGLPLSLAACRQMDVSVYLENPHQPSLQA | 240 |
| QY | 241 | TDSQGNVTLHALVMI SDMSANIALVMSXGGLQAGARLCPTVQLIEDIRNLQDLPLTK | 3000 |
| Db | 241 | TDSQGNVTLHALVMI SDMSANIALVMSXGGLQAGARLCPTVQLIEDIRNLQDLPLTK | 3000 |
| QY | 301 | AAKEKIEIFHHIILQREFSGLSHSRKFTEMWCYPRVRSYLDLASVSCSENSVLETTIAF | 3600 |
| Db | 301 | AAKEKIEIFHHIILQREFSGLSHSRKFTEMWCYPRVRSYLDLASVSCSENSVLETTIAF | 3600 |
| QY | 361 | HCKSPHRRHNVLEPLNKLLQAKMDLLIPKFLNLCNLVYMFIFTAVAHQPTLKKQA | 4200 |
| Db | 361 | HCKSPHRRHNVLEPLNKLLQAKMDLLIPKFLNLCNLVYMFIFTAVAHQPTLKKQA | 4200 |
| QY | 421 | PHLKAEVGNSMLLGHILLGGITLLVGGQMYWRKRHVFIMISFIDSYEILFLPQALL | 4800 |
| Db | 421 | PHLKAEVGNSMLLGHILLGGITLLVGGQMYWRKRHVFIMISFIDSYEILFLPQALL | 4800 |
| QY | 481 | TVVSOVLCEFLIEMVLPPLVSALVGMNLNLYYRGROHGTYSVMIOKYLIRDLRLEFL | 5400 |
| Db | 481 | TVVSOVLCEFLIEMVLPPLVSALVGMNLNLYYRGROHGTYSVMIOKYLIRDLRLEFL | 5400 |
| QY | 541 | TYLVFLFEGFAVALVSLSSEANRPAPPTGPNATESVOPMEQGEDEGNAOYRGILASLEL | 6000 |
| Db | 541 | TYLVFLFEGFAVALVSLSSEANRPAPPTGPNATESVOPMEQGEDEGNAOYRGILASLEL | 6000 |
| QY | 601 | FKEFTGMCELAFOQOLHFRGVALLLLAYVLLTYTILLNLIALMSTVSVATDSMSIV | 6600 |
| Db | 601 | FKEFTGMCELAFOQOLHFRGVALLLLAYVLLTYTILLNLIALMSTVSVATDSMSIV | 6600 |
| QY | 661 | KLQRAISYLEMENGYWMCRRKQORAGVMLTVGTRKDGSPDERMCRYEEVWMAWSMEQTLPT | 7200 |
| Db | 661 | KLQRAISYLEMENGYWMCRRKQORAGVMLTVGTRKDGSPDERMCRYEEVWMAWSMEQTLPT | 7200 |
| QY | 721 | LCEDPSGAGVPRTELENPVLASPKPEDEGDGASENYPVQLQSN 764 | |
| Db | 721 | LCEDPSGAGVPRTELENPVLASPKPEDEGDGASENYPVQLQSN 764 | |
| RESULT | 2 | | |
| QY9670 | | PRELIMINARY; PRT; 764 AA. | |
| AC | QY9670; | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Created) | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Last sequence update) | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | | |
| DE | VANILLOID RECEPTOR-LIKE PROTEIN. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Garcia R.L., Delmas P., Cesare P., England S., Liapi A., Wood J.N.; | | |
| RT | "Cloning and functional expression of VRL, a vanilloid receptor-like | | |
| RT | gene."; | | |
| RL | Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AF103906; AAD41724.1; - | | |
| DR | InterPro; IPR002110; - | | |
| DR | InterPro; IPR002111; - | | |
| DR | Pfam; PF00023; ank. 3. | | |
| DR | PROSITE; PSS0088; ANK_REPEAT. 1. | | |
| DR | PROSITE; PSS0297; ANK_REPEAT_REGION. 1. | | |
| DR | SMART; SM00248; ANK. 1. | | |
| DR | ReceptoF. | | |
| FW | | | |

| SEQ | SEQUENCE | 764 AA: | 86053 MM: | AF9DB8F495EB3A0 | CRC64: |
|-----------------------|--|--|---------------|-----------------|--------|
| Query Match | 98.5%; | Score 3945; | DB 4; | Length 764; | |
| Best Local Similarity | 98.2%; | Pred. No. 0; | | | |
| Matches 750; | Conservative | 6; | Mismatches 8; | Indels 0; | Gaps 0 |
| QY | 1 | MSPSSPVFRLETTLDGGDEGDESEADRGKLDYDGGSLPRMSESGPQGDGDRKFAQPIRVNLMV | 60 | | |
| DB | 1 | MSPSSSPVFRLETTLDGGDEGDESEADRGKLDYDGGSLPRMSESGPQGDGDRKFAQPIRVNLMV | 60 | | |
| QY | 61 | RKGTGASQDPDRPFDRDLRFNFVNSRCVPEDLGLPEYLSKTSKYLTDSYTEGSGTKCL | 120 | | |
| DB | 61 | RKGTGASQDPDRPFDRDLRFNFVNSRCVPEDLGLPEYLSKTSKYLTDSYTEGSGTKCL | 120 | | |
| QY | 121 | MKAVINLKDGVNACILPLLDIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSLOQCVK | 180 | | |
| DB | 121 | MKAVINLKDGVNACILPLLDIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSLOQCVK | 180 | | |
| QY | 181 | LLVENGANVHAACGRFPFGKGGTCTFYBEELPLSLAACKQMDVYSYLENHQPASLOA | 240 | | |
| DB | 181 | LLVENGANVHAACGRFPFGKGGTCTFYBEELPLSLAACKQMDVYSYLENHQPASLOA | 240 | | |
| QY | 241 | TDSQGTVYVHALVMTSDNSAENIALVTSWYDGLLOAGALCPVQEDIRNLQDLPLPL | 300 | | |
| DB | 241 | TDSQGTVYVHALVMTSDNSAENIALVTSWYDGLLOAGALCPVQEDIRNLQDLPLPL | 300 | | |
| QY | 301 | AAKEGKIEIFRRHILQREFSGLSHLNRKFFEMWCGYPAVRSVLYDLASVDSCEANSVLEIIAF | 360 | | |
| DB | 301 | AAKEGKIEIFRRHILQREFSGLSHLNRKFFEMWCGYPAVRSVLYDLASVDSCEANSVLEIIAF | 360 | | |
| QY | 361 | HCKSPHRRMNVLEPLNKLLOAKKMDLLPKFPLNLCNLIYMEIFTAVAYHOPTLKKQA | 420 | | |
| DB | 361 | HCKSPHRRMNVLEPLNKLLOAKKMDLLPKFPLNLCNLIYMEIFTAVAYHOPTLKKQA | 420 | | |
| QY | 421 | PLHKAEVGSMLLTGIIILLGGIYLVGQLMFWMRHVFIMISFDSYFELLFLPQALL | 480 | | |
| DB | 421 | PLHKAEVGSMLLTGIIILLGGIYLVGQLMFWMRHVFIMISFDSYFELLFLPQALL | 480 | | |
| QY | 481 | TIVSOVLCPALAEWYLPILVSALVIGWMLLKYTRGFQHTGYISVMIQKVIIRDLRLPFL | 540 | | |
| DB | 481 | TIVSOVLCPALAEWYLPILVSALVIGWMLLKYTRGFQHTGYISVMIQKVIIRDLRLPFL | 540 | | |
| QY | 541 | IYLVPLFGFAVALVLSLOEAPRPEAPPTGNATESVOPMGEODEGNGAORYGILLEASDEL | 600 | | |
| DB | 541 | IYLVPLFGFAVALVLSLOEAPRPEAPPTGNATESVOPMGEODEGNGAORYGILLEASDEL | 600 | | |
| QY | 601 | FEFTTGMGLAQOEDLHFRGMVLLLLLAVLLTYTILLNMLTALMSEYNSVATDSWSITW | 660 | | |
| DB | 601 | FEFTTGMGLAQOEDLHFRGMVLLLLLAVLLTYTILLNMLTALMSEYNSVATDSWSITW | 660 | | |
| QY | 661 | KLOKAIISVLEMENGVMWCKKORAGVMLTVGTRKPGSPDERMCCFRVEEYNMAASWEDTLPY | 720 | | |
| DB | 661 | KLOKAIISVLEMENGVMWCKKORAGVMLTVGTRKPGSPDERMCCFRVEEYNMAASWEDTLPY | 720 | | |
| QY | 721 | ICEDPSGAGVPTLENPVLASPPKEDDEGASENTPVQOLLOSN | 764 | | |
| DB | 721 | ICEDPSGAGVPTLENPVLASPPKEDDEGASENTPVQOLLOSN | 764 | | |
| RESULT | 3 | | | | |
| Q9WTR1 | PRELIMINARY; | PRT; | 756 AA. | | |
| AC | 01-NOV-1999 (TREMBLrel. 12, Created) | | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Last sequence update) | | | | |
| DE | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | | | | |
| BT | GROWTH FACTOR REGULATED CALCIUM CHANNEL. | | | | |
| GN | VR1 OR GRC. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| NC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57 BLACK-6; TISSUE=SPLEEN;
 RA Kanazaki M., Zhang Y., Kojima I.;
 RT "Growth factor regulated calcium channel.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021665; BAA78478.1; -
 DR MGI; MGI:1341836; Vrl.1.
 DR InterPro; IPR002110; -
 DR InterPro; IPR002111; -
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR SMART; SM00248; ANK; 1.
 SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EF4C CRC64;

Query Match 78.9%; Score 3159; DB 11; Length 756;
 Best Local Similarity 80.3%; Pred. No. 7.2e-241;
 Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSPPSPFRLFTLDGGDEGSEADRGKLDGSGGLPMEHQFQEDRKFAFOIRNLNY 60
 DB 1 MTSASNPAPFRLFTSDGDEGSAEVNKGK---NEPPMSEPFQEDRNFSPOIKYNLNY 56
 QY 61 RKGTGASQDPNRPDRDLFNVAVRGVPEDLAGLPEYLSKTSKYLTDSYTGSGTGKTL 120
 DB 57 RKGGLPSQDDPNRPDRDLFVSVRGVPEDLGLLEYLRKTSKYLTDSYTGSGTGKTL 116
 QY 121 MKAVINLKDGVNACILPLQLIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSLOCVK 180
 DB 117 MKAVINLKDGVNACILPLQLIDRDSGNPQPLVNAQCTDEFYRGHSAHIAIEKRSLOCVK 176
 QY 181 LLEVNGANVHAACGRFFKGGTCTFEGELPLSLAACKTQMDVYVYLLENHQPASLOA 240
 DB 177 LLEVNGANVHAACGRFFKGGTCTFEGELPLSLAACKTQMDVYVYLLENHQPASLOA 236
 QY 241 TDSQNTVYHALVMIISDNFAENIALVTSMYDGLDAGARLCTPVQEDIRNLQDILPLKL 300
 DB 237 TDSLQNTVYHALVMIISDNFAENIALVTSMYDGLDAGARLCTPVQEDIRNLQDILPLKL 296
 QY 301 AAKEGKIEIFRHILOREFSGI-SHSRKFTWCYGPVRAVSLYDLASVDSCEENSVLEIIA 359
 DB 297 AAKEGKIEIFRHILOREFSGIYQPLSRKFTWCYGPVRAVSLYDLASVDSCEENSVLEIIA 356
 QY 360 FHCKSPHRRHVRVLEPLNKLQAKMDLLPKFFLNLCULIYMTFTAVAYHOPTLKQA 419
 DB 357 FHCKSPHRRHVRVLEPLNKLQAKMDLLPKFFLNLCULIYMTFTAVAYHOPTLKQA 416
 QY 420 APHLKAENVNSMLTGHILLLGIGIYLVGOALWYFMRHVFYIWFISIDSYFELLFEOAL 479
 DB 417 TSSKATFEDSMILLGHILLLGIGIYLVGOALWYFMRHVFYIWFISIDSYFELLFEOAL 476
 QY 480 LTVNSQVLCFLAIEMYLPLVLSALVGLWMLNLLYTRGFQHTGYSVMIQKVLIRDLRL 539
 DB 477 LTVNSQVLCFLAIEMYLPLVLSALVGLWMLNLLYTRGFQHTGYSVMIQKVLIRDLRL 536
 QY 540 LLYLVFLFEGFANALVLSQSEAWRPEAPTPNATESYQPMEGQEDSCNGQYIGILEASLE 599
 DB 537 LLYLVFLFEGFANALVLSQSEAWRPEAPTPNATESYQPMEGQEDSCNGQYIGILEASLE 594
 QY 600 LKFTTGMGELAFOROLHRRGVNLLLLLYVLLTYILLNMLIALMSETVNSVATDSMGI 659
 DB 595 LKFTTGMGELAFOROLHRRGVNLLLLLYVLLTYILLNMLIALMSETVNSVATDSMGI 654
 QY 660 WKLOKAIIVLENGYVWCRKQ-RAGVNLVGTGKPDGSPDERMCFRVEVNWASWEQTL 718
 DB 655 WKLOKAIIVLENGYVWCRKQ-RAGVNLVGTGKPDGSPDERMCFRVEVNWASWEQTL 714
 QY 719 PTLCEPSSGAVPRLLENVYLASPKKEDDGSSEENVYVQILOSN 764
 DB 715 PTLCEPSSGAVPRLLENVYLASPKKEDDGSSEENVYVQILOSN 756

RESULT 4
 Q9WUD2 PRELIMINARY; PRT; 761 AA.
 AC Q9WUD2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
 GN VRL-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=99215558; PubMed=10201375;
 RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
 RT "A capsaicin-receptor homologue with a high threshold for noxious heat."
 RL Nature 398:436-441(1999).
 DR EMBL; AF129113; AAD26364.1; -
 DR InterPro; IPR002110; -
 DR InterPro; IPR002111; -
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR SMART; SM00248; ANK; 1.
 KW Receptor.
 SQ SEQUENCE 761 AA; 86689 MW; 46A281183EB672F CRC64;

Query Match 76.2%; Score 3051.5; DB 11; Length 761;
 Best Local Similarity 77.7%; Pred. No. 2.2e-232;
 Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSPPSPFRLFTLDGGDEGSEADRGKLDGSGGLPMEHQFQEDRKFAFOIRNLNY 60
 DB 1 MTSASNPAPFRLFTSDGDEGSAEVNKGK---NEPPMSEPFQEDRNFSPOIKYNLNY 56
 QY 61 ---RKGTGA-SQDPNRPDRDLFNVAVRGVPEDLAGLPEYLSKTSKYLTDSYTGSGT 115
 DB 57 IKRPKNTSAPSQQEDPNRPDRDLFVSVRGVPEDLGLLEYLRKTSKYLTDSYTGSGT 116
 QY 116 GKTCLMKAVNLKDGYNACILPLQLIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRS 175
 DB 117 GKTCLMKAVNLKDGYNACILPLQLIDRDSGNPQPLVNAQCTDEFYRGHSAHIAIEKRS 176
 QY 176 LQCVKLLENGANVHAACGRFFKGGTCTFEGELPLSLAACKTQMDVYVYLLENHQP 235
 DB 177 LQCVKLLENGANVHAACGRFFKGGTCTFEGELPLSLAACKTQMDVYVYLLENHQP 236
 QY 236 ASLOATDSQNTVYHALVMIISDNFAENIALVTSMYDGLDAGARLCTPVQEDIRNLQD 295
 DB 237 ASLEATDSQNTVYHALVMIISDNFAENIALVTSMYDGLDAGARLCTPVQEDIRNLQD 296
 QY 296 TPPLKLAAGKGIETFRHILOREFSG-LSHSRKFTWCYGPVRAVSLYDLASVDSCEENSV 354
 DB 297 TPPLKLAAGKGIETFRHILOREFSGYQPLSRKFTWCYGPVRAVSLYDLASVDSCEENSV 356
 QY 355 LELIAPHCKSPHRRHVRVLEPLNKLQAKMDLLPKFFLNLCULIYMTFTAVAYHOPT 414
 DB 357 LELIAPHCKSPHRRHVRVLEPLNKLQAKMDLLPKFFLNLCULIYMTFTAVAYHOPT 416
 QY 415 LKQAPHLKAENVNSMLTGHILLLGIGIYLVGOALWYFMRHVFYIWFISIDSYFELLF 474
 DB 417 LQOPALPSSKATFEGESMILLGHILLLGIGIYLVGOALWYFMRHVFYIWFISIDSYFELLF 476
 QY 475 LFOALLTVNSQVLCFLAIEMYLPLVLSALVGLWMLNLLYTRGFQHTGYSVMIQKVLIRDL 534
 DB 477 LFOALLTVNSQVLCFLAIEMYLPLVLSALVGLWMLNLLYTRGFQHTGYSVMIQKVLIRDL 536

| RESULT | 5 | | |
|--------|--|--------------|--------------|
| 09QYH8 | | | |
| ID | 09QYH8 | PRELIMINARY; | PRT; 761 AA. |
| AC | 09QYH8 | | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Created) | | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last sequence update) | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Last annotation update) | | |
| DE | STRETCH ACTIVATED CHANNEL 2B. | | |
| GN | RSAC2B. | | |
| OS | Rattus norvegicus (Rat) | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus | | |
| OX | NCBI_TaxID=10116; | | |
| RN | (1) | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Ishibashi K.; | | |
| RT | "Molecular cloning of a stretch activated channel from rat kidney."; | | |
| RL | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AB029330; BAA8637.1; -; | | |
| DR | InterPro; IPR002110; -; | | |
| DR | InterPro; IPR002111; -; | | |
| DR | Pfam; PF00023; ank; 3. | | |
| DR | PROSITE; PSS0088; ANK_REPEAT. 1. | | |
| DR | PROSITE; PSS0297; ANK_REPEAT_REGION. 1. | | |
| DR | SMART; SM00248; ANK; 1. | | |
| SQ | SEQUENCE 761 AA; 86705 MW; 8977CDE1D531EC8 CRC64; | | |

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0Y      1  MTSASSSVFRLERTLDGQEDGSEADNRKLLFGSLPPMSEQFGEDGRKFPQIRVNLN  60
      1  MTSASSSVFRLERTLDGQEDGSEADNRKLLFGSLPPMSEQFGEDGRKFPQIRVNLN  60
Db      1  MTSASSPFAFRLERTSDGEGEAGNAENKNGKQE----PPMSEPFQREDRNSSPQIRVNLNF  56
      1  MTSASSPFAFRLERTSDGEGEAGNAENKNGKQE----PPMSEPFQREDRNSSPQIRVNLNF  56
0Y      61  -----RKGTGA-SQDPDPNFDGDRLLFNNAVSGEVPEDLAGLPEYLSKTSKYLLDSEYTGST  119
      61  -----RKGTGA-SQDPDPNFDGDRLLFNNAVSGEVPEDLAGLPEYLSKTSKYLLDSEYTGST  119
      61  -----RKGTGA-SQDPDPNFDGDRLLFNNAVSGEVPEDLAGLPEYLSKTSKYLLDSEYTGST  119

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|----|-----|--|-----|
| QY | 116 | GKTCIMKRVVNLKQGVNACILPELLOIDRDSNPOLVNAOCTDDYVGHSHLHAIEKRS | 175 |
| Db | 117 | GKTCIMKRVVNLKQGVNACILPELLOIDRDSNPOLVNAOCTDDYVGHSHLHAIEKRS | 176 |
| QY | 176 | LQCVKLIVENGANYHARACGRFFQKGGCTCFYFGEELPLSLAAGTQMDVYVSYLLENHOP | 235 |
| Db | 177 | LQCVKLIVENGADYHLIRACGRFFQKHGCTCFYFGEELPLSLAAGTQMDVYVSYLLENHOP | 236 |
| QY | 236 | ASLOATDSQGNVTVLHALVMSDNSAENALVTSMTDGLLAGARLCPVVOLEDIRNLQDL | 295 |
| Db | 237 | ASLEATDSLGMTVTVLHALVMTADNSPENSALVIHYMTDGLLQMGARLCPVVOLEITSNQGL | 296 |
| QY | 296 | TPKLAAEKGIEIEFRHLOREFSG-LSHLSRKTETWCYGVVRSLVDLASVDSCEANSV | 354 |
| Db | 297 | TPKLAAEKGIEIEFRHLOREFSGPYQPSRKKTETWCYGVVRSLVDLASVDSOWENKSV | 355 |

| | | | |
|--------|--|--------------|--------------|
| RESULT | 6 | | |
| 09JMI8 | | | |
| ID | 09JMI8 | PRELIMINARY; | PRT; 762 AA. |
| AC | 09JMI8 | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TReMBLrel. 15, last sequence update) | | |
| DT | 01-MAR-2001 (TReMBLrel. 16, last annotation update) | | |
| DE | ION CHANNEL. | | |
| OS | Rattus norvegicus (Rat). | | |
| CC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eueleostomi; | | |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus | | |
| OX | NCBI_Taxid=10116; | | |
| LN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=KIDNEY; | | |
| RA | Suzuki M.; | | |
| RT | "Ion channel."; | | |
| RL | Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AB022332; BAA93435.1; -. | | |
| DR | InterPro; IPR002110; -. | | |
| DR | InterPro; IPR002111; -. | | |
| DR | Pfam; PF00023; ank. 3. | | |
| DR | PROSITE; PSS0088; ANK_REPEAT. 1. | | |
| DR | PROSITE; PSS0297; ANK_REPEAT_REGION. 1. | | |
| DR | SMART; SM00248; ANK. 1. | | |
| QO | SEQUENCE 762 AA; 86767 MW; CE0970BC4195351E CRC64; | | |

[illegible]

Qy 116 GKTCLMKAVALNLKDGYNACIIPLLQIDRDSGNQPLVNAQCTDYYRGHSLHIAIEKRS 175
 |||||
 Db 117 GKTCLMKAVALNLQDGNACIIPLLQIDKDSGNKLLVNAQCTDEYYQGHSLHIAIEKRS 176


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Db 157 SELLTHKKRLTDEEFREPSTGKTCPLKALLNLSAGRNDTIPILLDIAEKTKGNMREFINSP 216
Qy 156 CTDDYVRGSHALIAIERKSLQCVKLLVNGANVHARACGRFQ--KGQCTCFPGGLPS 214
Db 217 FRVYVYRGOTAHIAIERCKKHVVELVERGADVAGRFQPPDEGFFYFGLPLS 276
Qy 215 LAACQOMPVSYLBNPQASLOATDSOGNTVLHALVMSIDNSMENIALYTSMTDGL 274
Db 277 LAACQOMPHIVHLETLNGKQADLRQDSRGNTVLHALVAIDNTENKRFYTKMDLL 336
Qy 275 QAGARLCPTVOLEDIRNLQDLPPLKLAKEGKIEIFRHILQREFS--GLSHLSRKFTMC 332
Db 337 IKCARLSEPTNLLEALLNNDCLSPDMAAKTGKIGIFQHIIRREIAEDVYRHLSRKTKDMA 396
Qy 333 YGPRVRSLYDLASVSC--EENSVLELIAFHCKSPHRRHNVLEPLKLLQAKKDL--IRK 390
Db 397 YGPRVRSLYDLASVSC--EENSVLELIAFHCKSPHRRHNVLEPLKLLQAKKDL--IRK 390
Qy 391 PFLNFCNLTYMFIFPAVYHOPTLKKQAAPHLKAEVGNMILTGILLGLGTYLLVGQ 450
Db 457 FETSVSYLCAMITFLIAYRP--MEGPPRYTTTIDYLRAGETITLLIGILFEFFSN 514
Qy 451 LW-YEMRRHVFIMISFIDSYFELLFLQALLTVVSGVLCFLAIEWYLPPLVSALVGMWN 509
Db 515 IKDLFMKKGPGVNSPFIIDGSPFQLYEYSVLVITAGLYGVEAYLVAVFALVGMWN 574
Qy 510 LLYTTPGPHGTGYSWMIOKVILRLRLLYLVLFEGFANALVL-----SDE 559
Db 575 ALYFTRGTLGTYSIMIKILFKDLFRLLYLLFMIMYASALVSLNCPSSSESCSD 634
Qy 560 AMREAPTPGNATESVQPMEOGDEGNGAQYRGLLEASLELEFRTGMELAFQOLHFR 619
Db 635 HSNCTIPTYPSCRDS-----QTFSTFLDLDFKLTIGMGDLEMLSAKIP 678
Qy 620 GAVLLLLAYVLLTYLLNLMLALMSETVNSVADSWMSIMLOKAISVLEMENGY--MMC 678
Db 679 GVEIILLVYIILTFVLLNMLALMGEITVGQVSKESKHIMKQWATITLIDERSFPL 738
Qy 679 RKORAGVNLVTGTRKDGSPDERMCRVEEVNMAWEOQLPTLCEPDSAG----- 729
Db 739 RRAFSGEMVYVKGKTDGTPDRRMCRFVDEVMNSHWNQNLGITSEDPGKSDTYQYGFESH 798
Qy 730 -----VPRLENPVLASPPKED 746
Db 799 TVGRLRRDRMSTVPRVVE--LNKSCPTED 826

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RESULT 14
Q9HBC0 PRELIMINARY; PRT; 871 AA.

AC 09HBC0: 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL CORTEX;
RX PubMed=11025659;
RA Stromann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.:
RT "ORPDC4, a nonselective cation channel that confers sensitivity to
extracellular osmolarity".
RL Nat. Cell Biol. 2:695-702(2000).
DR Emb. AF258465; AAG16127.1;
SQ SEQUENCE 871 AA; 98294 MW; C62056B8D6A6FB6 CRC64;

Query Match 36.6%; Score 1467; DB 4; Length 871;
Best Local Similarity 43.1%; Pred. No. 3.4e-107;

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Matches 339; Conservative 114; Mismatches 246; Indels 88; Gaps 16;
Qy 8 PVFRLETLUGGQEDG-----SEADRGK-LDFGSLPMPESQFQEDKRP----- 52
Db 32 PLSLNLNLEEG--EDGLSPSPADASRPAGPGRPLRMKFGQAFKGPVNPIDLESTL 90
Qy 53 -----QIRVNLNRYK-----GTGASOPDP--NRPD 75
Db 91 YESSVPGCKKAPMDSLFDTGYTRHHSNDKRWKKIIEKQPOSAPAPAPDPPILKVFN 150
Qy 76 RDLFNVAASRGVPEDLAGEPEYLSKTSKYLTDSYEGSTGKTCMLKAVNLKDGVNACI 135
Db 151 RLPLFDIVYRGSTADLDGLPLFLTHKKRLTDEEFREPSTGKTCPLKALLNLSNGNDTI 210
Qy 136 LPLQIDRDSGNPQPLVNAQCTDDYVRGSHALIAIERKSLQCVKLLVNGANVHARAC 195
Db 211 PVLIDIAERTGNMREFINSPFRDIYRGOTAHIAIERCKKHVVELLVAGADVHAQAG 270
Qy 196 RFPQ--KGQCTCFYFGLPLSLAICTQMPDVSYLBNPQASLOATDSOGNTVLHALV 254
Db 271 RFPQKDEGFFYFGLPLSLAICTQMPHIVNLTPHKKADMRQDSRGNTVLHALVA 330
Qy 255 ISDNSAENIALYTSMTDGLQAGARLCPTVOLEDIRNLQDLPPLKLAKEGKIEIFRHIL 314
Db 331 IADNTENKRFYTKMYDILLKCARLPDSNLEAVLNNDCLSPDMAAKTGKIGIFQHI 390
Qy 315 QREFS--GLSHLSRKFTMCYGPVRSLYDLASVSC--EENSVLELIAFHCKSPHRRHNV 371
Db 391 RREVYDEDRHLSRKTKFDMAVGPVRSLYDLASVSLDSCGEASVLELYVNSKIENHEML 450
Qy 372 VLEPLKLLQAKKDL--IPKFLNFCNLTYMFIFPAVYHOPTLKKQAAPHLKAEVGN 430
Db 451 AVEPIINELLRDKKRGKGAVSFIINVSYLCANVIFLTYQPL--EGTPPYRYRTTVY 508
Qy 431 MLTGHILLGLGTYLLVGLQW-YEMRRHVFIMISFIDSYFELLFLQALLTVVSGVLCF 489
Db 509 LRLAGEVITLFGVLPFFFNIKDLFMKKGPGVNSPFIIDGSPFQLYEYSVLVVSALVL 568
Qy 490 LAIEWLPLPLVSALVGMNLVYTRGPHGTGYSWMIOKVILRLRLLYLVLFEGF 549
Db 569 AGTEAVLAVNALVGMNALLYTRGLKLTGTYSIMIKILFKDLFRLLYLLFMICY 628
Qy 550 AVALVSL-----SDEAMREAPTPGNATESVQPMEOGDEGNGAQYRGLLEASLE 599
Db 629 ASALVSLNLPKANMKACNEDQNTCTPYTPSCRDS-----ETFSFL---LD 672
Qy 600 LRFETIGMELAFQEOHLHFGVNLVLLAYVLLTYLLNLMLALMSETVNSVADSWMSI 659
Db 673 LFLITIGMGDLEMLSTKYPVVFIIILTYIILTFVLLNMLALMGEITVGQVSKESKH 732
Qy 660 WKLOKAISVLEMENGY--MMCRRKORAGVNLVTGTRKDGSPDERMCRVEEVNMAWEOQL 718
Db 733 WKLOWATITLIDERSFPVLRKAFRSGEMVYVKGKSDGTPDRMCRFVDEVMNSHWNQNL 792
Qy 719 PTLCEDP 725
Db 793 GIINEDP 799

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RESULT 15
Q9ER28 PRELIMINARY; PRT; 871 AA.

AC 09ER28: 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
GN VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN 111

RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX Pubmed=11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
Sali A., Hudspeth A.J., Friedman J.M., Heller S.,
RT "Vanilloid receptor-related osmotically activated channel (VR-ORC), a
candidate vertebrate osmoreceptor.";
RT Cell 103:525-535(2000).
DR EMBL; AF263521; AAG28027.1; -.
KW Receptor.
SQ SEQUENCE 871 AA: 98009 MW: 5D50684DA08C354B CRC64;

Query Match 36.6%; Score 1465.5; DB 11; Length 871;
Best Local Similarity 40.4%; Pred. No. 4.5e-107;
Matches 341; Conservative 128; Mismatches 257; Indels 119; Gaps 16;

QY 8 PVPRLETLGGCGEDGS-----EADRGKLDPGSGLPMEGSGFQGEDRKFP-----52
DB 32 PLSSLANLEEGEGSSSLSPVDASR--PAGPGDGRPNLRMKFGCAFRRKGVNPIIDLESTL 90
QY 53 -----QIRVNLNVRKRGTCGASQDPENR-----FD 75
DB 91 YESSVYPPGKKAPMDSLFDYGYTRHHPSDKKRRKRVVEKQPOSKAPAPQPPILKVEN 150
QY 76 RDRLEFNAVSGVPEDLAGLPEYLKSTSKYLTDSYEGSTGKTCLMKAVLNLDKGVNACI 135
DB 151 RPILFDIYVSRGTSADLDGLLSTLTGKRLTDEFEFREPSTGCTCLPALLNLNNGRNDTI 210
QY 136 LPLLDIDRDSGNPQPLVNAOCTDDYRGHSALHIAIEKRSLOCVKLLVENGANVHARACG 195
DB 211 PVLIDIAERTGNMREINSPFDIYRGQTLHIAIERCKHYVELLVAGADVHAQARG 270
QY 196 RFEQ--KGQGTCEYFEGELPTSLACTKQWVSYLLENPHOPASLOATDSOGNTVLHAIY 254
DB 271 RFPQPKDEGTYFEGELPLSLACTQPHIVNLTENPHKADMRDSDRGNTVLHALVA 330
QY 255 ISDNSAENIALVTSMYDGLLAGARLPTVOLEDINLQDLTPLKLAEGKTEIFRHIL 314
DB 331 IADNTRENTKFTYKMYDLLLKCSRLFPDSNLETVLNNDGLSPLMAAKTGKIGVQHII 390
QY 315 QREFS--GSHLSRKTENCYGPVRSYLDLASVDSG--EENSYLELIAFHCSPHRHRV 371
DB 391 RREYVDEDTRHLSRRKKDMAYGVSYSLLDSCGEGSVYLETLVYNSKIENHEML 450
QY 372 VLEPLKRLQAKKDLL--IKFELNFCNLTYEIFTAVAYHOPTLKKQAAPHLKAEVGS 430
DB 451 AVEPIELLRDKKRRKGAVSFYINVSYLCAMVITFLTAYQPL--EGTPPIYRTTVDY 508
QY 431 MLTGHILLILGGIYLVGOLW--YEMRRHVFIMSFIDSYFEILLFLOALLTVVSOVLGF 489
DB 509 LRLAGEVITLLGVLEFFTSIKDLFMKCPGVNSLEFVDSGFLQFYISVLVVSAALYL 568
QY 490 LAIEWLPLPLVSAIVGMNLXYTRGFQHTGYSVMIOKAVILRDLRLFLIYVFLSGF 549
DB 569 AGIEALVAVPALVIGMNAALYFTRGKLTGYTSMIQKILFKDLFRLLVLYLLEFMIGY 628
QY 550 AVALVSL-----SOEAMRPEAPTPGNATESVQPMEGDEGNGAQYRGITLASLE 599
DB 629 ASALVITLLNPCINMKVCNEDQNCYFSTPACRDS-----ETFSAFI--LD 672
QY 600 LRFKTIQMGELAFQDLHRGAVLLLLLVVLLTYILLNMLIALMSETVNSVATDSMSI 659
DB 673 LFKLTIGMDLMLSSAKYPVVEFILLVYIILTFVLLNMLIALMGETVGQVSKESKHI 732
QY 660 WKLOKAISYLEMENGY--WCCRKKQKAGVMLYVTKPDGSDERKCFRVEEVNMAWSEOTL 718
DB 733 WKLOWATITLIDERSPPVLRKAFRSGEVMTVGKSSDGTDDRRCQFRYDEVNMSHNQNL 792
QY 719 PFLCEDPS-----GAGVPRITLENPVLASPRKDEGASSEENVY 756
DB 793 GIINEDPGKSEIYQYYGFSHTMGRLRDRWSSVPRVVE-----LNKNSGIDEVVV 843

QY 757 PVQLL 761
DB 844 PLDNL 848

Search completed: July 18, 2001, 16:00:08
Job time: 136 sec